

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:02 ; Search time 299.73 Seconds  
(without alignments)  
26.982 Million cell updates/sec

Title: US-09-331-631A-1\_COPY\_117\_185

Perfect score: 384  
Sequence: 1 NR0RDP00QYEQCQKHCORR.....EEQREDEKYEERMKREDN 69

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_15:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	666	10 Q9SP15	Q9SP15 macadamia i
2	367	95.6	666	10 Q9SP14	Q9SP14 macadamia i
3	363	94.5	625	10 Q9SP13	Q9SP13 macadamia i
4	172	44.8	525	10 Q43358	Q43358 theobroma c
5	163	42.4	593	10 Q9SEW4	Q9SEW4 juglans reg
6	120.5	31.4	554	5 Q9VPS3	Q9VPS3 drosophila
7	116.5	30.3	1038	5 Q60983	Q60983 dictyosteli
8	115	29.9	1089	12 Q40947	Q40947 kaposi's sa
9	114	27.9	810	10 Q9ZWI3	Q9ZWI3 cucurbita m
10	107	27.9	1162	12 Q98148	Q98148 kaposi's sa
11	105.5	27.5	1129	12 Q9OR71	Q9OR71 kaposi's sa
12	105	27.3	1737	5 Q9TW28	Q9TW28 dictyosteli
13	104.5	27.2	385	5 Q17909	Q17909 caenorhabdi
14	104	27.1	1390	5 Q77033	Q77033 dictyosteli
15	103	26.8	838	5 Q9YOC9	Q9YOC9 dictyosteli
16	101	26.3	233	4 Q9UFP2	Q9UFP2 homo sapien
17	101	26.3	289	4 Q9NUN6	Q9NUN6 homo sapien
18	101	26.3	1027	4 Q9NST7	Q9NST7 homo sapien
19	101	26.3	1165	4 Q95819	Q95819 homo sapien

20	101	26.3	1175	4 Q75172	Q75172 homo sapien
21	101	26.3	1233	11 P97820	P97820 mus musculu
22	101	26.3	1257	4 Q95033	Q95033 homo sapien
23	100.5	26.2	489	10 Q9SP11	Q9SP11 glycine max
24	100.5	26.2	2123	5 Q9U9S7	Q9U9S7 dictyosteli
25	99.5	25.9	2701	4 Q9V520	Q9V520 homo sapien
26	98.5	25.7	1268	4 Q9UKD8	Q9UKD8 homo sapien
27	98.5	25.7	1276	4 Q9UKD1	Q9UKD1 homo sapien
28	98.5	25.7	1297	4 Q9UKD9	Q9UKD9 homo sapien
29	98.5	25.7	1305	4 Q9UKD3	Q9UKD3 homo sapien
30	98.5	25.7	1323	4 Q9UKD0	Q9UKD0 homo sapien
31	98.5	25.7	1333	4 Q9UKD4	Q9UKD4 homo sapien
32	98.5	25.7	1331	4 Q60298	Q60298 homo sapien
33	98.5	25.7	1352	4 Q9UKD2	Q9UKD2 homo sapien
34	98.5	25.7	1360	4 Q9UKD5	Q9UKD5 homo sapien
35	98.5	25.7	1700	5 Q9VVA9	Q9VVA9 drosophila
36	98	25.5	648	5 Q9TXB8	Q9TXB8 dictyosteli
37	98	25.5	876	11 Q9WU62	Q9WU62 mus musculu
38	97	25.3	503	5 Q25777	Q25777 plasmodium
39	96.5	25.1	1125	5 Q9W3X0	Q9W3X0 drosophila
40	96	25.0	479	5 Q9U380	Q9U380 caenorhabdi
41	96	25.0	652	4 Q15410	Q15410 homo sapien
42	96	25.0	2023	4 Q75557	Q75557 homo sapien
43	96	25.0	2023	4 Q9UND7	Q9UND7 homo sapien
44	96	25.0	2212	4 Q9UHV6	Q9UHV6 homo sapien
45	95.5	24.9	171	11 Q61118	Q61118 mus musculu

## ALIGNMENTS

RESULT 1  
Q9SP15 PRELIMINARY: PRT: 666 AA.  
AC Q9SP15;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE VICILIN PRECURSOR.  
GN AMP2.  
OS Macadamia integrifolia (Macadamia nut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
OC NCBI\_TaxID=60698;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=NOT KERNEL.  
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;  
RT "A family of antimicrobial peptides is produced by processing of a 7S  
RT globulin protein in Macadamia integrifolia kernels.";  
RL Plant J. 0:0-0(1999).  
DR EMBL: AF161883; A054244.1; -.  
DR HSSP: P02853; 2PHL.  
DR INTERPRO: IPR001113; -.  
DR PFM: PF00546; Seedstore\_7s; 1.  
SQ SEQUENCE 666 AA: 78217 MW: C752B884B2DF0224 CRC64;

Query Match 100.0%; Score 384; DB 10; Length 666;  
Best local Similarity 100.0%; Pred. No. 5.2e-27;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NR0RDP00QYEQCQKHCORRERPRHMOTCCQRCFRYERKKKKRREDEKEXY 60  
DB 117 NR0RDP00QYEQCQKHCORRERPRHMOTCCQRCFRYERKKKKRREDEKEXY 176  
QY 61 EERMKREDN 69  
DB 177 EERMKREDN 185  
RESULT 2  
Q9SP14

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ID 09SPL4 PRELIMINARY: PRT: 666 AA.
AC 09SPL4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
  globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999)
DR EMBL: AF161884; AAD54245.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA; 78243 MW; 0ECA22F8710F8A7B CRC64;

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Query Match 95.6%; Score 367; DB 10; Length 666;
Best Local Similarity 95.7%; Pred. No. 1.7e-25;
Matches 66; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 NRORPQOQYEOCQKRCORRETPRHMOJCQRCERREYKERRKQOQRYEEOQREDEEKY 60
DB 117 NRORPQOQYEOCQKRCORRETPRHMOJCQRCERREYKERRKQOQRYEEOQREDEEKI 176
OY 61 EERMKEDN 69
DB 177 EERMKEDN 185

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RESULT 3
ID 09SPL3 PRELIMINARY: PRT: 625 AA.
AC 09SPL3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
  globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999)
DR EMBL: AF161885; AAD54246.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
FT NON_TER 1
SQ SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

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```

Query Match 94.5%; Score 363; DB 10; Length 625;
Best Local Similarity 95.7%; Pred. No. 3.7e-25;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 NRORPQOQYEOCQKRCORRETPRHMOJCQRCERREYKERRKQOQRYEEOQREDEEKY 60
DB 76 NRORPQOQYEOCQKRCORRETPRHMOJCQRCERREYKERRKQOQRYEEOQREDEEKI 135

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OY 61 EERMKEDN 69
DB 136 EERMKEDN 144

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RESULT 4
ID 043358 PRELIMINARY: PRT: 525 AA.
AC 043358:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 13, Last annotation update)
DE VICILIN PRECURSOR.
GN CSV.
OS Theobroma cacao (Cacao).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Theobroma.
OX NCBI_TaxID=3641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAVES;
RA MEDLINE=92288309; PubMed=1600151;
RA McHenry L., Filtz P.J.;
RT "Comparison of the structure and nucleotide sequences of vicilin genes
  of cocoa and cotton raise questions about vicilin evolution.";
RL Plant Mol. Biol. 18:1173-1176(1992).
DR EMBL: X62625; CAA44493.1; -
DR EMBL: X62626; CAA44494.1; -
DR HSSP: P02853; 2PHL.
DR MENDEL: 30919; Thecc; 1188; 30919.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
DR PRODOM: PD081059; -; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 525 VICILIN.
SQ SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;

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Query Match 44.8%; Score 172; DB 10; Length 525;
Best Local Similarity 31.4%; Pred. No. 3.1e-08;
Matches 32; Conservative 20; Mismatches 14; Indels 36; Gaps 2;

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OY 3 QRPDQOQYEOCQKRCORRETPRHMOJCQRCERREYKERRKQOQRYEEOQREDEEKY 46
DB 35 ERPRDQOQYEOCQKRCSEATREERQECQRCERREYKERRKQOQRYEEOQREDEEKY 94
OY 47 -----KRYEEOQREDEEKY---EERMKED 68
DB 95 QDQGREQOQOCCQKRCWEQYKQDQRCHEVYHNHKNRSEEE 136

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RESULT 5
ID 09SEW4 PRELIMINARY: PRT: 593 AA.
AC 09SEW4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fagales; Juglandaceae; Juglans.
OX NCBI_TaxID=51240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE;
RA Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
RT "Identification and cloning of a cDNA encoding a vicilin-like protein,
  Jug r 2, from English walnut kernel (Juglans regia): a major food

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09OR71
ID 09OR71 PRELIMINARY; PRT; 1129 AA.
AC 09OR71;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE LATENT NUCLEAR ANTIGEN.
GN ORF 73.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GX18;
RA Glenn M., Rainbow L., Aurade F., Davison A., Schulz T.F.;
RT "Identification of a Spliced Gene from Kaposi's Sarcoma-Associated
RT Herpesvirus Encoding a Protein with Similarities to Latent Membrane
RT Proteins 1 and 2A of Epstein-Barr Virus.";
RL J. Virol. 73:6953-6963(1999).
DR EMBL: AF148805; AAD46501.1; -.
DR INTERPRO: IPR000533; -.
DR INTERPRO: IPR002017; -.
DR INTERPRO: IPR002965; -.
DR PRINTS: PR00194; TROPOMYOSIN.
DR PRINTS: PR01217; PRICHEXTENSIN.
SQ SEQUENCE 1129 AA; 131346 MW; 8F63855B45F79109 CRC64;

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```

Query Match 27.5%; Score 105.5; DB 12; Length 1129;
Best Local Similarity 31.9%; Pred. No. 0.046;
Matches 22; Conservative 24; Mismatches 20; Indels 3; Gaps 1;

QY 2 RORPPOOYEQCCKHRCRRETEPRHMO---TCOORCERRYEKKRKOORKEOQREDEE 58
   1:||||| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
Db 612 QOQDEQOQDEQOQDEQOQDEQOQDEQOQDEQOQDEQOQDEQOQDEQOQDEQOQDEQ 671
   1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
QY 59 KYERKKEE 67
   1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
Db 672 QOQDEQOQDEQ 680

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RESULT 12
09TW28
ID 09TW28 PRELIMINARY; PRT; 1737 AA.
AC 09TW28;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE MYOM PROTEIN.
GN MYOM.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RA Oishi N., Adachi H., Sutoh K.;
RT "Dictyostelium discoideum gene for Myom.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RA Geissler H., Schwarz E.C., Soldati T.;
RT "Identification of two novel and highly divergent myosins in
RT Dictyostelium discoideum.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB01910; BAAB4604.1; -.
DR EMBL: AF090533; AAD47903.1; -.
DR HSSP: P08799; 1MND.
DR INTERPRO: IPR000194; -.
DR INTERPRO: IPR000219; -.
DR INTERPRO: IPR001609; -.

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DR INTERPRO: IPR001849; -.
DR PFAM: PF00063; myosin_head; 2.
DR PFAM: PF00169; PH; 1.
DR PFAM: PF00621; RhogGFP; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
SQ SEQUENCE 1737 AA; 195860 MW; 39CBF9C08BFF856 CRC64;

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Query Match 27.3%; Score 105; DB 5; Length 1737;
Best Local Similarity 36.2%; Pred. No. 0.073;
Matches 25; Conservative 20; Mismatches 20; Indels 4; Gaps 2;

QY 1 NRORPPOOYEQCCKHRCRRETEPRHMO---TCOORCERRYEKKRKOORKEOQREDEE 59
   1:||||| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
Db 940 NKREKEERKE---LERORKEEREROKELERORKEERELERORKEERELERORKEER 996
   1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
QY 60 YEERKKEED 68
   1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
Db 997 EQERKKEE 1005

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RESULT 13
Q17909
ID Q17909 PRELIMINARY; PRT; 385 AA.
AC Q17909;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE C11G6.3 PROTEIN.
GN C11G6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; Pubmed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Straden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z70204; CAA94113.1; -.
DR INTERPRO: IPR001965; -.
DR PRAM: PF00628; PHD; 1.
SQ SEQUENCE 385 AA; 46052 MW; D080FC63B47EDC1 CRC64;

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Query Match 27.2%; Score 104.5; DB 5; Length 385;
Best Local Similarity 27.6%; Pred. No. 0.024;
Matches 21; Conservative 24; Mismatches 22; Indels 9; Gaps 1;

QY 2 RORPPOOYEQCCKHRCRRETEPRHMO-----TCOORCERRYEKKRKOORKEOQREDEE 52
   1:||||| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
Db 146 RERERKREERERERERERERERERERERERERERERERERERERERERERERERER 205
   1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
QY 53 QREDEKYEERKKEED 68
   1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:| 1:|
Db 206 LKKEKSEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKE 221

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Search completed: March 1, 2001, 16:09:05  
Job time: 1549 sec

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RESULT 14
ID 077033 PRELIMINARY: PRT: 1390 AA.
AC 077033;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DE 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE TRFA.
GN TRFA.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RA Saito J., Adachi H., Sutoh K.;
RT "Dictyostellium TRFA homologous to yeast Snf6 is required for normal
RT growth and early development.";
RL J. Biol. Chem. 0:0-0(1998).
DR EMBL; AB009080; BAA33143.1; -.
DR INTERPRO: IPR001440; -.
DR PFAM: PF00515; TPR: 9.
SQ SEQUENCE 1390 AA; 160421 MW; BAA89926656002DE CRC64;

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Query Match 27.1%; Score 104; DB 5; Length 1390;
Best Local Similarity 23.9%; Pred. No. 0.075;
Matches 16; Conservative 30; Mismatches 21; Indels 0; Gaps 0;

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QY 2 RQRPQOQYEQCKHCQRETEPRHMQCQKCEKRYEKKRQKRYEQREDEEKEYE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 91 QQQQPPQQQSSQQQQQQQQQQQQQQPPQQQQPPQQQQQQPPQQQQQQQQQQPPQQ 150
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 ERMKKEED 68
DB 151 QQQQQQQD 157

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RESULT 15
ID 09Y0C9 PRELIMINARY: PRT: 838 AA.
AC 09Y0C9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE RAS INTERACTING PROTEIN RIPA.
GN RIPA.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee S., Parent C.A., Inasal R., Firtel R.A.;
RT "The novel ras interacting protein required for chemotaxis and cAMP
RT signal relay in Dictyostellium.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159241; AAD43567.1; -.
SQ SEQUENCE 838 AA; 94059 MW; EAAD911294226808 CRC64;

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Query Match 26.8%; Score 103; DB 5; Length 838;
Best Local Similarity 23.9%; Pred. No. 0.061;
Matches 16; Conservative 33; Mismatches 18; Indels 0; Gaps 0;

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QY 1 NRQRDPQOQYEQCKHCQRETEPRHMQCQKCEKRYEKKRQKRYEQREDEEKEYE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 88 NQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQ 147
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 EERMKKEE 67
DB 148 QVQAQQQ 154

```